

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 22:20:37 ; Search time 8376 Seconds  
(without alignments)  
11511.938 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcgccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	% Query					Description
	No.	Score	Match Length	DB	ID	
	1	2357	100.0	2357	6	AX225986 Sequence
	2	2289.6	97.1	2459	6	AX713908 Sequence
	3	2289.6	97.1	2459	9	AK055829 Homo sapi
	4	2285.2	97.0	2370	6	AX451429 Sequence
	5	2236.6	94.9	2535	9	BC037291 Homo sapi
	6	2236.2	94.9	2481	6	AX451427 Sequence
	7	2235.6	94.8	2528	9	AK096021 Homo sapi
	8	2018.6	85.6	2351	6	AX225978 Sequence
	9	1910.2	81.0	1926	6	AX226045 Sequence
	10	1788.8	75.9	2294	9	AK092526 Homo sapi
	11	1307.4	55.5	1373	9	AF258588 Homo sapi
	12	967.8	41.1	4120	9	AB011181 Homo sapi
	13	967.8	41.1	4326	9	HSA7583 Homo sapi
	14	935.4	39.7	3669	10	MMAJ6278 Mus muscu
	15	935.4	39.7	4746	10	AK122328 Mus muscu
	16	665.8	28.2	1113	10	BC033922 Mus muscu
	17	470	19.9	171115	9	AC068385 Homo sapi
c	18	223.8	9.5	190937	2	AC103477 Rattus no
	19	223.8	9.5	220358	2	AC129036 Rattus no
c	20	217.4	9.2	211034	10	AL731709 Mouse DNA
c	21	159.2	6.8	60579	9	HS282F2 Human DNA
	22	157	6.7	157	6	AX226018 Sequence
c	23	147	6.2	118914	2	AC079554 Mus muscu
c	24	147	6.2	197270	2	AC139293 Mus muscu
	25	142.2	6.0	231844	2	AC116068 Rattus no
	26	136.6	5.8	153451	2	AC079576 Mus muscu
	27	118.6	5.0	157	6	AX226019 Sequence
c	28	101	4.3	37731	9	HSB1D7 Human DNA s
	29	95.2	4.0	171504	2	AC115798 Mus muscu
c	30	95.2	4.0	234234	2	AC097194 Rattus no
c	31	94.2	4.0	10620	9	HSN4F11 Human DNA s
	32	92.4	3.9	1869	6	AX054959 Sequence
c	33	91.6	3.9	153451	2	AC079576 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 23:35:18 ; Search time 610 Seconds  
(without alignments)  
10430.452 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcggccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:\*
- 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:\*
- 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:\*
- 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2357	100.0	2357	22	AAD15483	Human NOVX7 DNA fr	
2	2285.2	97.0	2370	24	AAD35231	Human TRNFR-16 cDN	
3	2236.2	94.9	2481	24	AAD35229	Human TRNFR-14 cDN	
4	2018.6	85.6	2351	22	AAD15479	Human NOVX3 DNA fr	
5	1910.2	81.0	1926	22	AAD15502	Human NOVX7 DNA in	
6	1490.2	63.2	2368	24	ABL35093	Murine cDNA isolat	
7	1307.4	55.5	1373	24	ABL50341	Human cancer cell	
8	1121.2	47.6	1366	21	AAC76301	Human ORFX ORF1856	
9	967.8	41.1	4142	19	AAV62750	Human secreted pro	
10	967.8	41.1	4142	24	ABQ92053	Human polynucleoti	
11	967.8	41.1	4326	23	AAS69668	DNA encoding novel	
12	914.2	38.8	4037	23	AAS69666	DNA encoding novel	
13	913.4	38.8	2082	23	AAS69667	DNA encoding novel	
c 14	316	13.4	316	24	ABL87371	Human ovarian canc	
15	294.8	12.5	354	24	ABZ08305	Human leukocyte de	
16	176.4	7.5	349	22	ABA11735	Human nervous syst	
c 17	104.4	4.4	248	22	ABA50408	Human breast cell	
c 18	104.4	4.4	248	22	ABA35355	Probe #13821 for g	
c 19	104.4	4.4	248	22	AAK16732	Human brain expres	
20	92.4	3.9	1869	22	AAC90954	C. elegans I-beta-	
21	68.6	2.9	1513	21	AAC59566	Human secreted pro	
22	66	2.8	408	23	AAS69669	DNA encoding novel	
23	57.2	2.4	965	24	ABQ54340	Human ovarian anti	
24	56	2.4	1387	22	AAC89050	Human insulin-like	
25	56	2.4	1387	24	ABN95846	Gene #2344 used to	
26	56	2.4	1387	24	ABL68139	Kidney cancer rela	
27	56	2.4	1433	17	AAQ99243	Insulin like growt	
28	56	2.4	1433	22	AAF45142	IGFBP-2 coding seq	
29	56	2.4	1433	25	ACC46776	Human COPD related	
30	56	2.4	1433	25	ABX76314	Lung cancer-associ	
31	56	2.4	1433	25	ABV75369	Human IGFBP-2 poly	
32	56	2.4	1438	11	AAQ04550	EcoRI-EcoRI fragme	
c 33	55.2	2.3	380	22	ABA45273	Human breast cell	
c 34	55.2	2.3	380	22	ABA25445	Probe #3911 for ge	
c 35	55.2	2.3	380	22	AAK03983	Human brain expres	
c 36	52.8	2.2	77536	21	AAA14651	Nucleotide sequenc	
c 37	51	2.2	2918	21	AAZ43922	S. tendae nikkomyc	
38	50	2.1	50	24	ABZ05039	Human leukocyte ge	
c 39	50	2.1	50	24	ABZ06750	Human leukocyte ge	
40	50	2.1	50	24	ABZ07140	Human leukocyte ge	
c 41	50	2.1	50	24	ABZ07434	Human leukocyte ge	
42	50	2.1	50	24	ABZ07513	Human leukocyte ge	
c 43	49	2.1	8438	15	AAQ73500	DNA encoding Pseud	
44	48.6	2.1	1248	22	AAC90937	Human i-beta-1,3-N	
45	48.6	2.1	2011	20	AAX99465	Beta 1,3-N-acetylgl	

# ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 23:47:28 ; Search time 164 Seconds  
(without alignments)  
6343.537 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcgccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
	Query	Match	Length	DB	ID		
No.	Score						
	1	56	2.4	1433	2	US-08-666-392A-1	Sequence 1, Appli
	2	56	2.4	1433	3	US-09-199-926-1	Sequence 1, Appli
c	3	52.8	2.2	77536	4	US-09-410-551B-1	Sequence 1, Appli
	4	49.8	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c	5	49	2.1	8438	1	US-07-945-283-1	Sequence 1, Appli
	6	48.6	2.1	2011	4	US-09-182-450-2	Sequence 2, Appli
c	7	47.4	2.0	651	4	US-09-252-991A-2095	Sequence 2095, Ap
	8	44.8	1.9	2401	3	US-09-320-878-20	Sequence 20, Appl
	9	44.8	1.9	2401	4	US-09-141-908-9	Sequence 9, Appli
	10	44.8	1.9	2401	4	US-09-657-440-20	Sequence 20, Appl
	11	44.8	1.9	2430	3	US-09-105-537-23	Sequence 23, Appl

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OM nucleic - nucleic search, using sw model

Run on: February 14, 2004, 02:29:08 ; Search time 819 Seconds  
(without alignments)  
10601.126 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcgcccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2289.6	97.1	2459	13	US-10-094-749-592	Sequence 592, App
2	2285.2	97.0	2370	13	US-10-288-252-36	Sequence 36, Appl
3	2236.2	94.9	2481	13	US-10-288-252-34	Sequence 34, Appl
4	2235.6	94.8	2516	13	US-10-301-822-66	Sequence 66, Appl
5	2235.6	94.8	2528	12	US-10-108-260A-1027	Sequence 1027, Ap
6	1788.8	75.9	2294	12	US-10-104-047-1109	Sequence 1109, Ap
7	1490.2	63.2	2368	11	US-09-866-050A-622	Sequence 622, App
8	1490.2	63.2	2368	15	US-10-152-661-622	Sequence 622, App
9	1031.2	43.8	1339	13	US-10-305-810-2	Sequence 2, Appli
10	967.8	41.1	4142	9	US-09-745-763-141	Sequence 141, App
c 11	316	13.4	316	10	US-09-867-701-10349	Sequence 10349, A
12	294.8	12.5	354	12	US-10-131-827-8296	Sequence 8296, Ap
c 13	282.8	12.0	737	13	US-10-027-632-22209	Sequence 22209, A
c 14	282.8	12.0	737	14	US-10-027-632-22209	Sequence 22209, A
15	213.6	9.1	549	13	US-10-027-632-276046	Sequence 276046,
16	213.6	9.1	549	14	US-10-027-632-276046	Sequence 276046,
17	153.6	6.5	415	10	US-09-783-590-2422	Sequence 2422, Ap
c 18	104.4	4.4	248	9	US-09-864-761-20675	Sequence 20675, A
c 19	74.4	3.2	536	13	US-10-029-386-60	Sequence 60, Appl
c 20	74.4	3.2	551	13	US-10-029-386-10461	Sequence 10461, A
21	72.4	3.1	757	13	US-10-027-632-26463	Sequence 26463, A
22	72.4	3.1	757	13	US-10-027-632-26464	Sequence 26464, A
23	72.4	3.1	757	13	US-10-027-632-149804	Sequence 149804,
24	72.4	3.1	757	14	US-10-027-632-26463	Sequence 26463, A
25	72.4	3.1	757	14	US-10-027-632-26464	Sequence 26464, A
26	72.4	3.1	757	14	US-10-027-632-149804	Sequence 149804,
c 27	71.4	3.0	210	13	US-10-029-386-13767	Sequence 13767, A
28	57.2	2.4	965	12	US-10-264-049-220	Sequence 220, App
29	56.2	2.4	684	13	US-10-027-632-104108	Sequence 104108,
30	56.2	2.4	684	13	US-10-027-632-324966	Sequence 324966,
31	56.2	2.4	684	14	US-10-027-632-104108	Sequence 104108,
32	56.2	2.4	684	14	US-10-027-632-324966	Sequence 324966,
33	56	2.4	1387	10	US-09-880-107-2344	Sequence 2344, Ap
34	56	2.4	1433	11	US-09-791-196-1	Sequence 1, Appli
35	56	2.4	1433	12	US-10-159-563-28	Sequence 28, Appl
36	56	2.4	1433	13	US-10-133-937-28	Sequence 28, Appl
c 37	55.2	2.3	380	9	US-09-864-761-3911	Sequence 3911, Ap
c 38	52.8	2.2	77536	13	US-09-940-316B-1	Sequence 1, Appli
39	50	2.1	50	12	US-10-131-827-5030	Sequence 5030, Ap
c 40	50	2.1	50	12	US-10-131-827-6741	Sequence 6741, Ap
41	50	2.1	50	12	US-10-131-827-7131	Sequence 7131, Ap
c 42	50	2.1	50	12	US-10-131-827-7425	Sequence 7425, Ap
43	50	2.1	50	12	US-10-131-827-7504	Sequence 7504, Ap
44	48.6	2.1	2011	13	US-10-166-098-2	Sequence 2, Appli
45	48.6	2.1	2011	15	US-10-171-581-71	Sequence 71, Appl

## ALIGNMENTS

RESULT 1  
US-10-094-749-592

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 23:37:32 ; Search time 4437 Seconds  
(without alignments)  
12910.897 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcggccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*



28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1508	64.0	2384	14	CB605771	CB605771 AMGNNUC:M
	2	1367.4	58.0	2310	11	AK077630	AK077630 Mus muscu
c	3	878.4	37.3	1047	13	BX361329	BX361329 BX361329
	4	853.2	36.2	1052	13	BX361330	BX361330 BX361330
c	5	830	35.2	1201	13	BX381996	BX381996 BX381996
	6	750.6	31.8	1201	13	BX381997	BX381997 BX381997
	7	747.6	31.7	801	13	BU568646	BU568646 AGENCOURT
	8	744.4	31.6	758	10	BG743518	BG743518 602635548
	9	743.2	31.5	789	12	BM008947	BM008947 603618754
	10	698.2	29.6	735	9	AW177915	AW177915 IL3-HT006
	11	669.6	28.4	687	9	AW177916	AW177916 IL3-HT006
	12	669.2	28.4	675	9	AW177837	AW177837 IL3-HT005
c	13	664	28.2	1153	13	BX339192	BX339192 BX339192
	14	652.6	27.7	915	13	BQ920751	BQ920751 AGENCOURT
c	15	645.8	27.4	724	9	AW177914	AW177914 IL3-HT006
	16	631.6	26.8	689	9	AW177912	AW177912 IL3-HT006
c	17	628.4	26.7	632	9	AW272738	AW272738 xu22b04.x
	18	617.6	26.2	718	9	AW177972	AW177972 IL3-HT006
	19	600.6	25.5	1063	11	BC004023	BC004023 Mus muscu
	20	595.4	25.3	619	10	BG112663	BG112663 602282217
c	21	591.2	25.1	597	9	AW177925	AW177925 IL3-HT006
c	22	584.2	24.8	637	9	AW177918	AW177918 IL3-HT006
c	23	578	24.5	695	9	AW361936	AW361936 PM3-CT026
	24	571.4	24.2	612	9	AW365272	AW365272 MR0-HT006
	25	569.6	24.2	851	12	BI452835	BI452835 603170364
	26	566.8	24.0	670	9	AW178028	AW178028 IL3-HT006
c	27	563.6	23.9	632	10	BF349160	BF349160 IL3-HT006
	28	553.6	23.5	839	10	BF538203	BF538203 602053675
c	29	552.6	23.4	577	9	AI739555	AI739555 wi35a01.x
c	30	549	23.3	551	9	AI890442	AI890442 wm85d10.x
	31	543	23.0	594	9	AW177976	AW177976 IL3-HT006
c	32	533	22.6	591	9	AW662322	AW662322 hi23f09.x
	33	527.8	22.4	652	10	BF046368	BF046368 BP250021A
c	34	527.8	22.4	686	9	AW177984	AW177984 IL3-HT006
c	35	524	22.2	524	9	AI554243	AI554243 tq15g03.x
	36	523.2	22.2	732	9	AW178024	AW178024 IL3-HT006
c	37	522	22.1	534	9	AI972669	AI972669 wr41g08.x
	38	509.8	21.6	666	9	AW178030	AW178030 IL3-HT006
c	39	505.6	21.5	557	9	AW365441	AW365441 MR0-HT007
c	40	504.8	21.4	518	9	AW166756	AW166756 xg77a08.x
	41	498.4	21.1	542	13	BQ322349	BQ322349 QV1-CS000
c	42	497.6	21.1	632	9	AW365197	AW365197 MR0-HT006
	43	497.4	21.1	902	12	BI656699	BI656699 603283862
	44	495.2	21.0	765	12	BI151421	BI151421 602917419
c	45	492.6	20.9	507	10	BF349158	BF349158 IL3-HT006

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 23:57:14 ; Search time 6509 Seconds  
(without alignments)  
12009.069 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcgggcgccatg.....attaaagttttaaaacatca 2357

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1.	2357	100.0	2357	1	PCT-US03-03401-149	Sequence 149, App
2	2357	100.0	2357	1	PCT-US03-03401A-149	Sequence 149, App
3	2357	100.0	2357	2	PCT-US03-03401-149	Sequence 149, App
4	2357	100.0	2357	2	PCT-US03-03401A-149	Sequence 149, App
5	2357	100.0	2357	33	US-09-783-436-13	Sequence 13, Appl
6	2357	100.0	2357	33	US-09-783-436A-13	Sequence 13, Appl
7	2357	100.0	2357	42	US-09-970-813A-13	Sequence 13, Appl
8	2289.6	97.1	2459	1	PCT-US03-03401-141	Sequence 141, App
9	2289.6	97.1	2459	1	PCT-US03-03401A-141	Sequence 141, App
10	2289.6	97.1	2459	2	PCT-US03-03401-141	Sequence 141, App
11	2289.6	97.1	2459	2	PCT-US03-03401A-141	Sequence 141, App
12	2289.6	97.1	2459	45	US-10-094-749-592	Sequence 592, App
13	2285.2	97.0	2370	49	US-10-288-252-36	Sequence 36, Appl
14	2237.2	94.9	2521	1	PCT-US02-41825-259	Sequence 259, App
15	2237.2	94.9	2521	50	US-10-335-053-259	Sequence 259, App
16	2236.6	94.9	2666	48	US-10-214-831-1	Sequence 1, Appli
17	2236.6	94.9	2666	86	US-60-311-150-1	Sequence 1, Appli
18	2236.2	94.9	2481	49	US-10-288-252-34	Sequence 34, Appl
19	2235.6	94.8	2516	1	PCT-US02-37431-66	Sequence 66, Appl
20	2235.6	94.8	2516	50	US-10-301-822-66	Sequence 66, Appl
21	2235.6	94.8	2528	46	US-10-108-260A-1027	Sequence 1027, Ap
22	2228.6	94.6	3042	1	PCT-US03-03401-139	Sequence 139, App
23	2228.6	94.6	3042	1	PCT-US03-03401A-139	Sequence 139, App
24	2228.6	94.6	3042	2	PCT-US03-03401-139	Sequence 139, App
25	2228.6	94.6	3042	2	PCT-US03-03401A-139	Sequence 139, App
26	2176.8	92.4	2680	26	US-09-606-680-3355	Sequence 3355, Ap
27	2176.8	92.4	2680	26	US-09-607-200-7459	Sequence 7459, Ap
28	2176.8	92.4	2680	26	US-09-616-081-1274	Sequence 1274, Ap
29	2176.8	92.4	2680	30	US-09-698-010-11812	Sequence 11812, A

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OM nucleic - nucleic search, using sw model

Run on: February 14, 2004, 02:18:54 ; Search time 821 Seconds  
(without alignments)  
8428.566 Million cell updates/sec

Title: US-09-783-436A-13  
Perfect score: 2357  
Sequence: 1 cgcccccgctcggcggccatg.....attaaagtttttaaaacatca 2357

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4928475 seqs, 1467936547 residues

Total number of hits satisfying chosen parameters: 9856950

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
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7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq2:\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2357	100.0	2357	7	US-10-357-885-149	Sequence 149, App
2	2289.6	97.1	2459	7	US-10-357-885-141	Sequence 141, App
3	2228.6	94.6	3042	7	US-10-357-885-139	Sequence 139, App
4	2137.4	90.7	2549	7	US-10-357-885-137	Sequence 137, App
5	2133.8	90.5	2857	7	US-10-357-885-135	Sequence 135, App
6	2132.2	90.5	2897	1	PCT-US03-30720-85	Sequence 85, Appl
7	2091.2	88.7	2450	1	PCT-US03-23249-81	Sequence 81, Appl
8	2028	86.0	2105	7	US-10-357-885-143	Sequence 143, App
9	2024.8	85.9	2094	7	US-10-357-885-153	Sequence 153, App